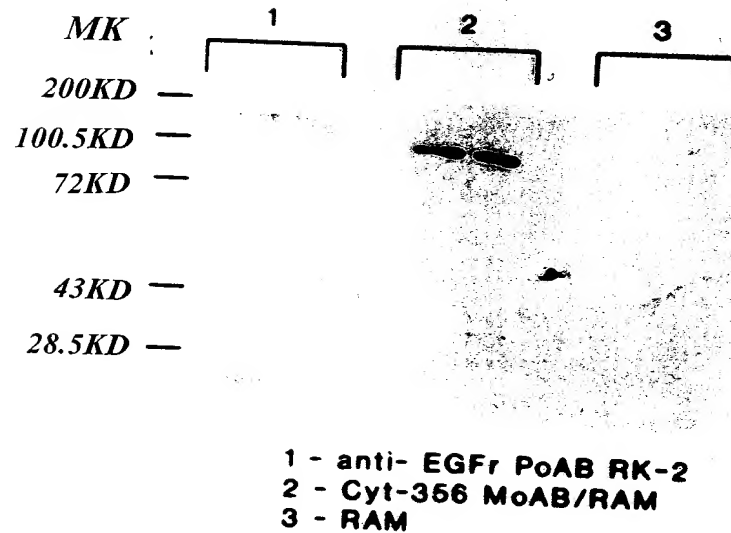




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**FIGURE 1**



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BEST AVAILABLE COPY

FIGURE 2B



FIGURE 2A



FIGURE 2D



FIGURE 2C



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FIGURE 3B

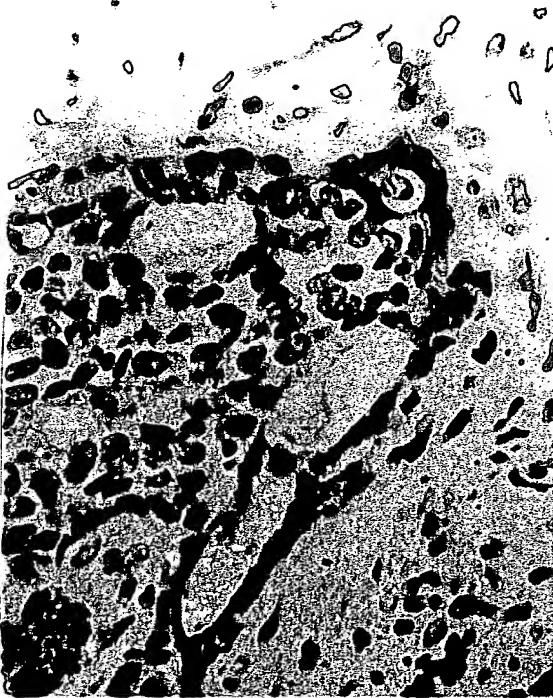


FIGURE 3D



FIGURE 3A

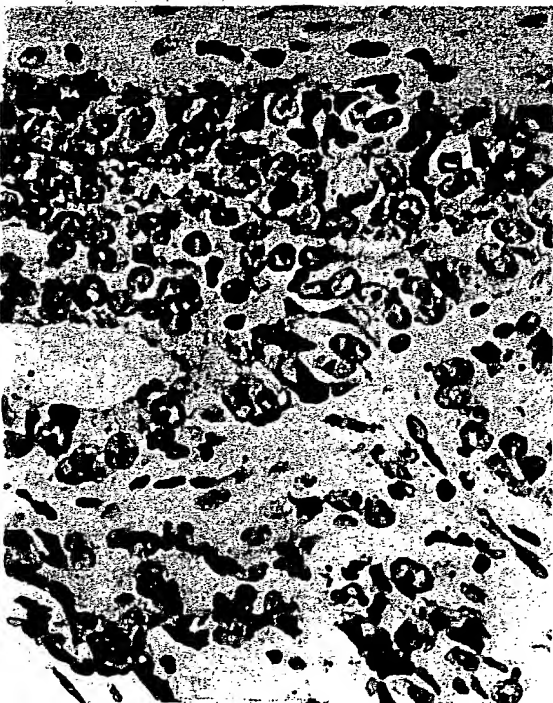
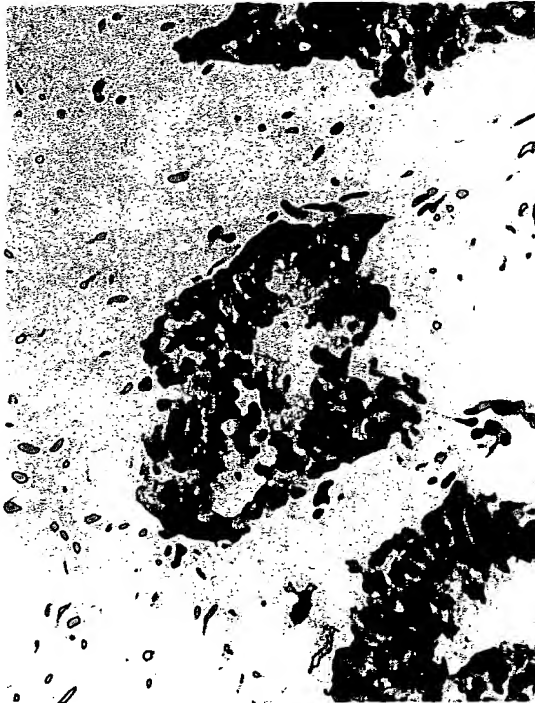
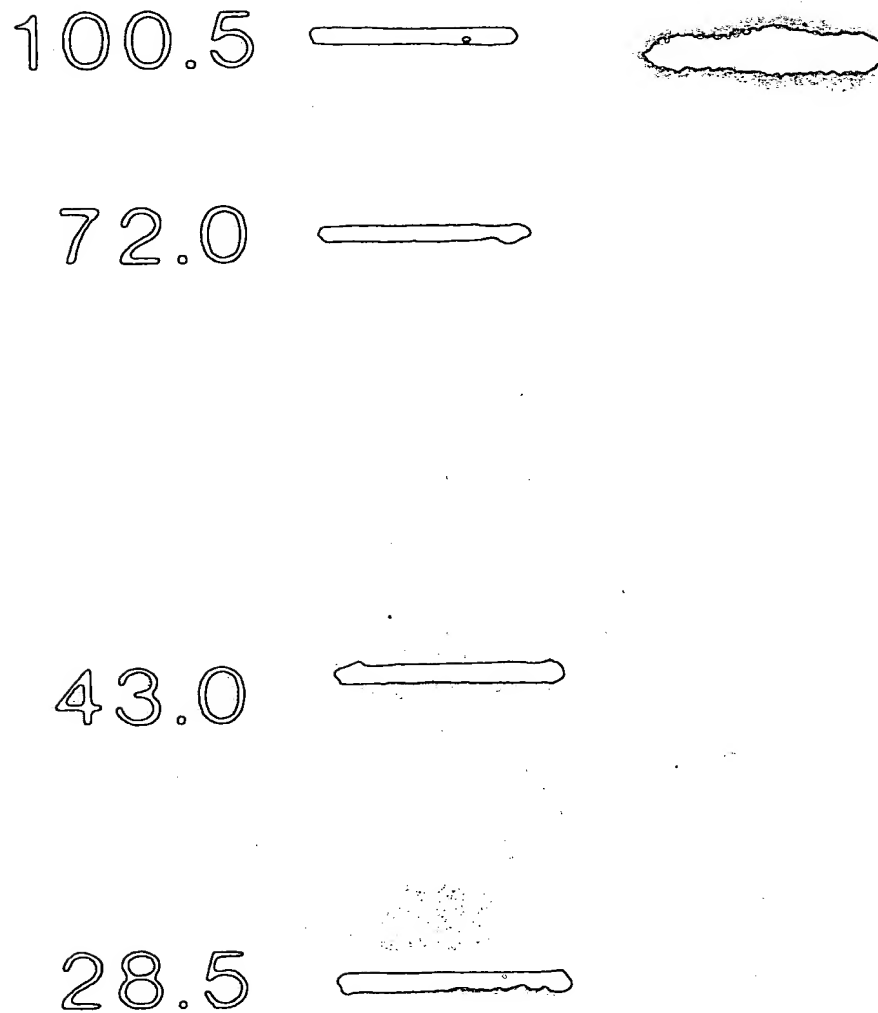


FIGURE 3C



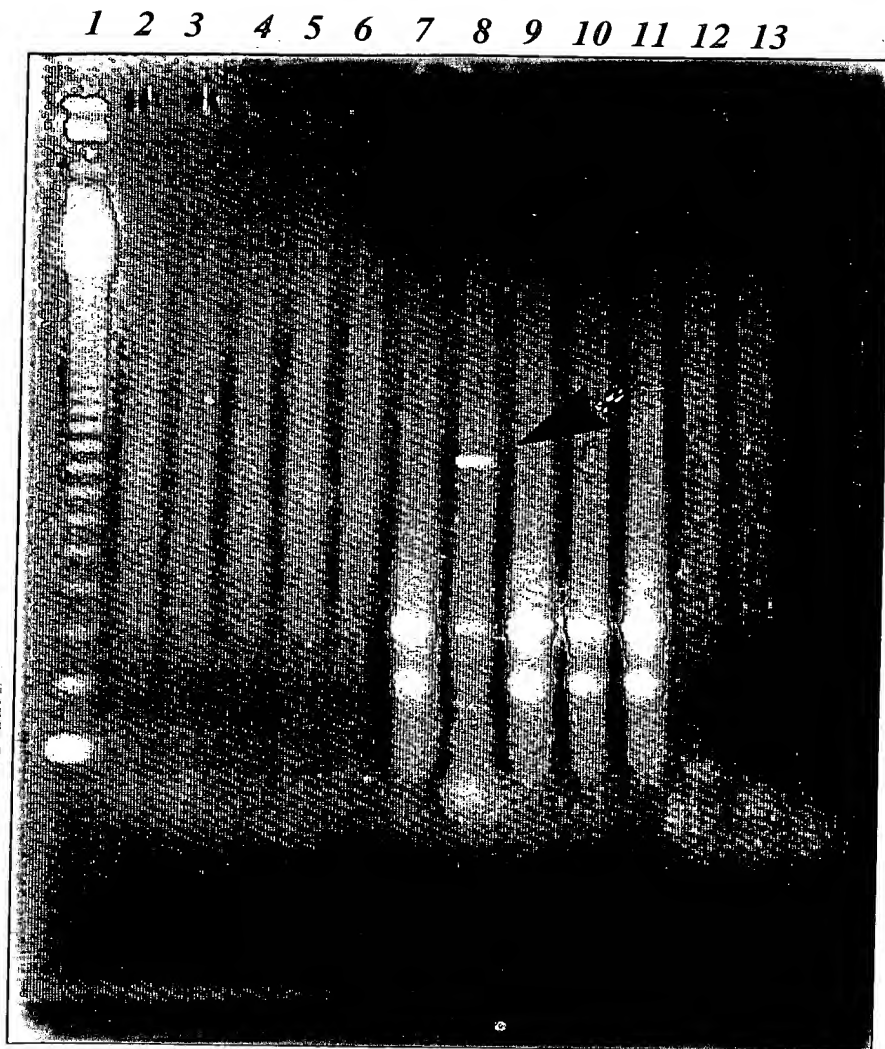
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FIGURE 4



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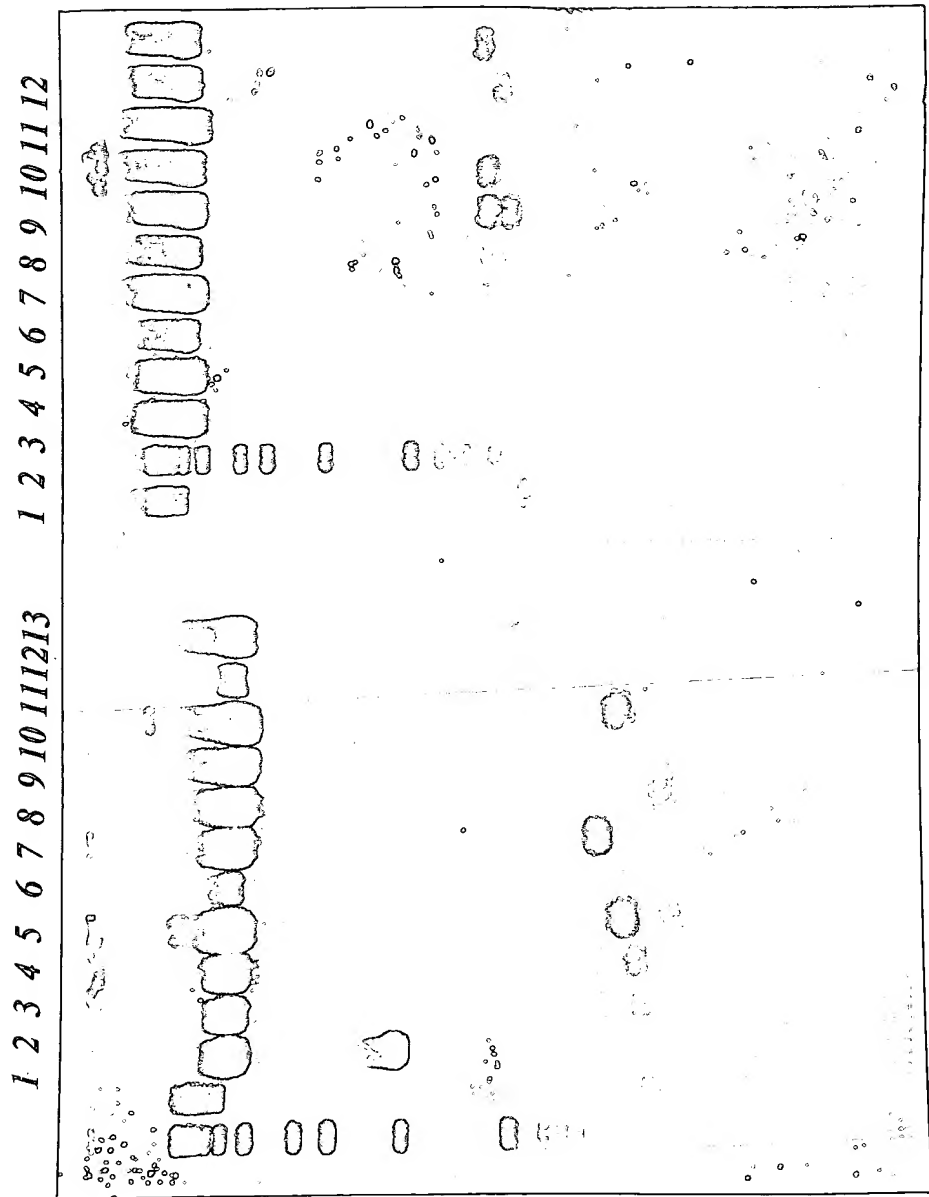
FIGURE 5



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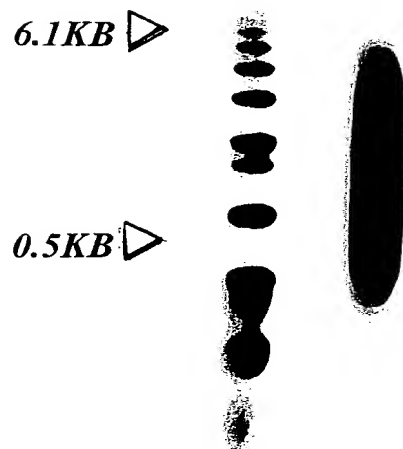
FIGURE 6A

FIGURE 6B



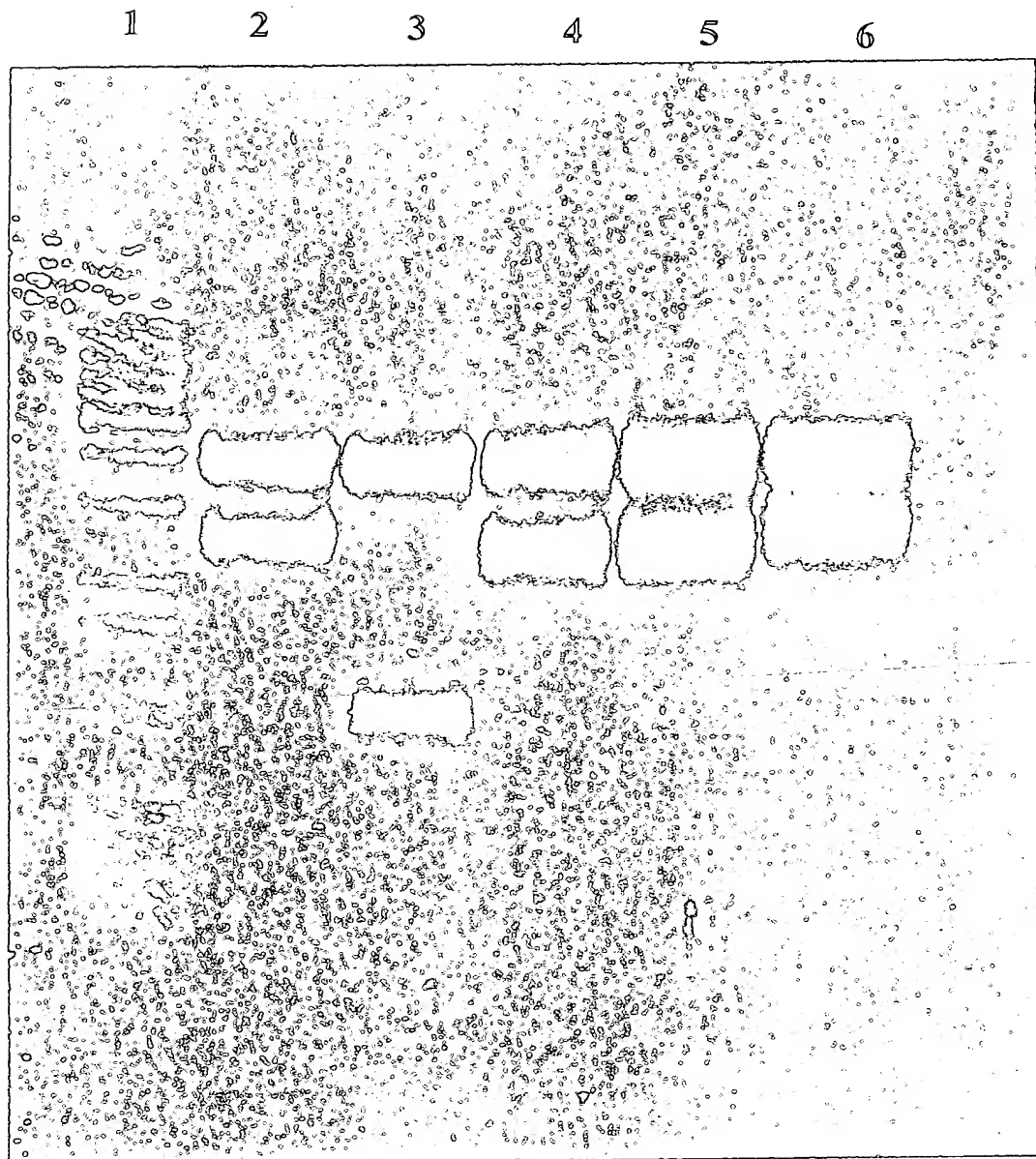
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**FIGURE 7**



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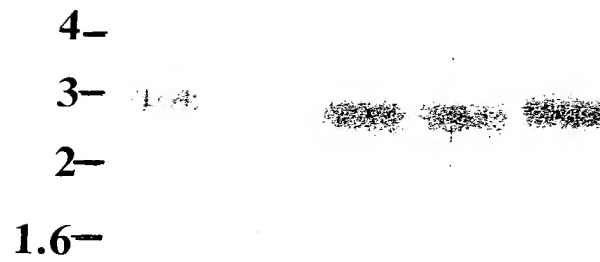
FIGURE 8





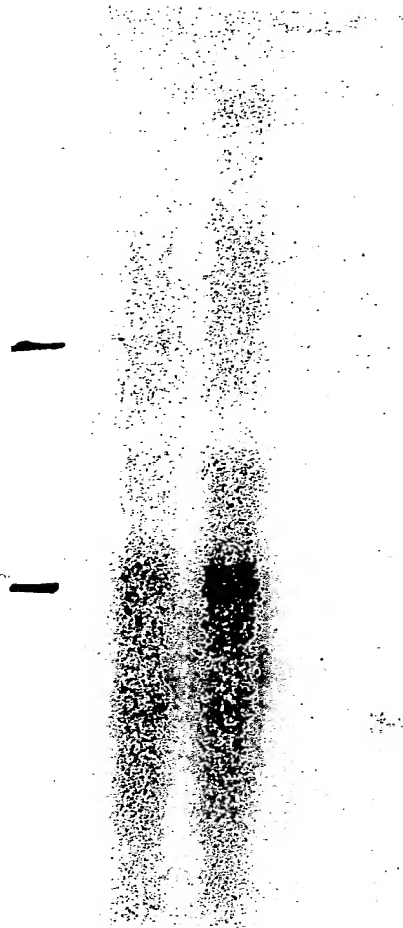
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**FIGURE 9**



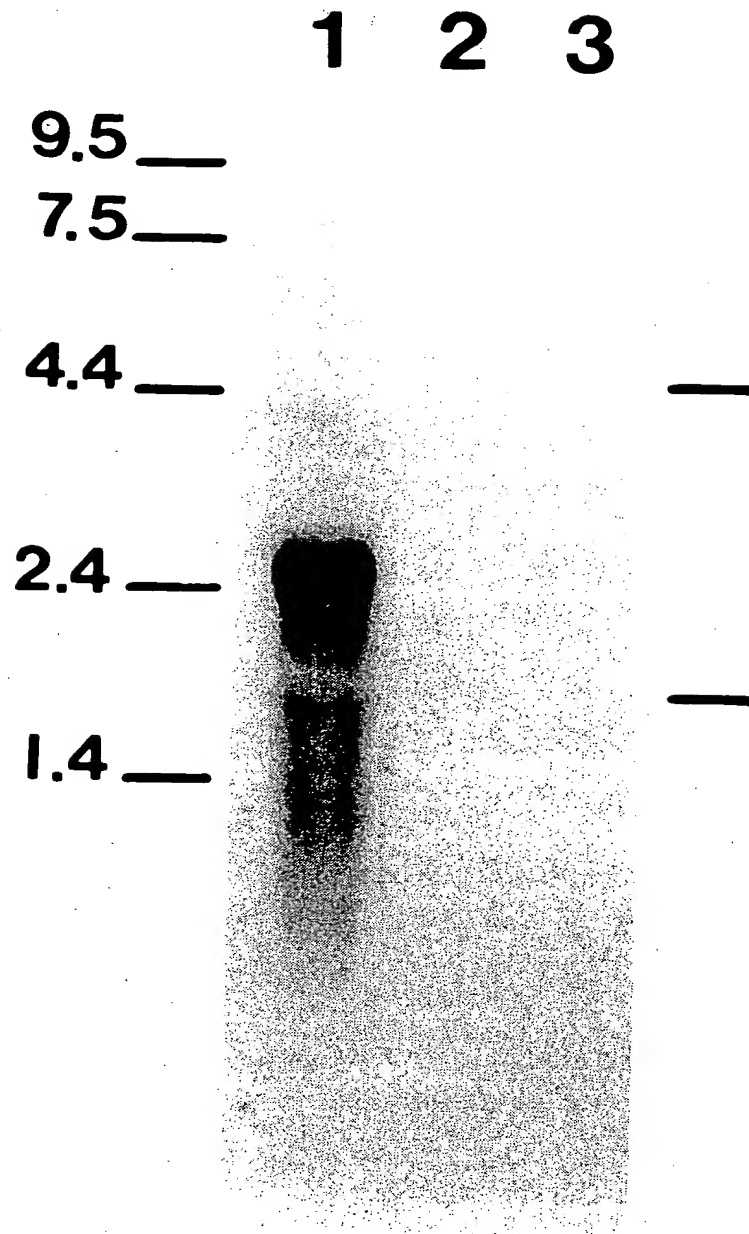
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***FIGURE 10***



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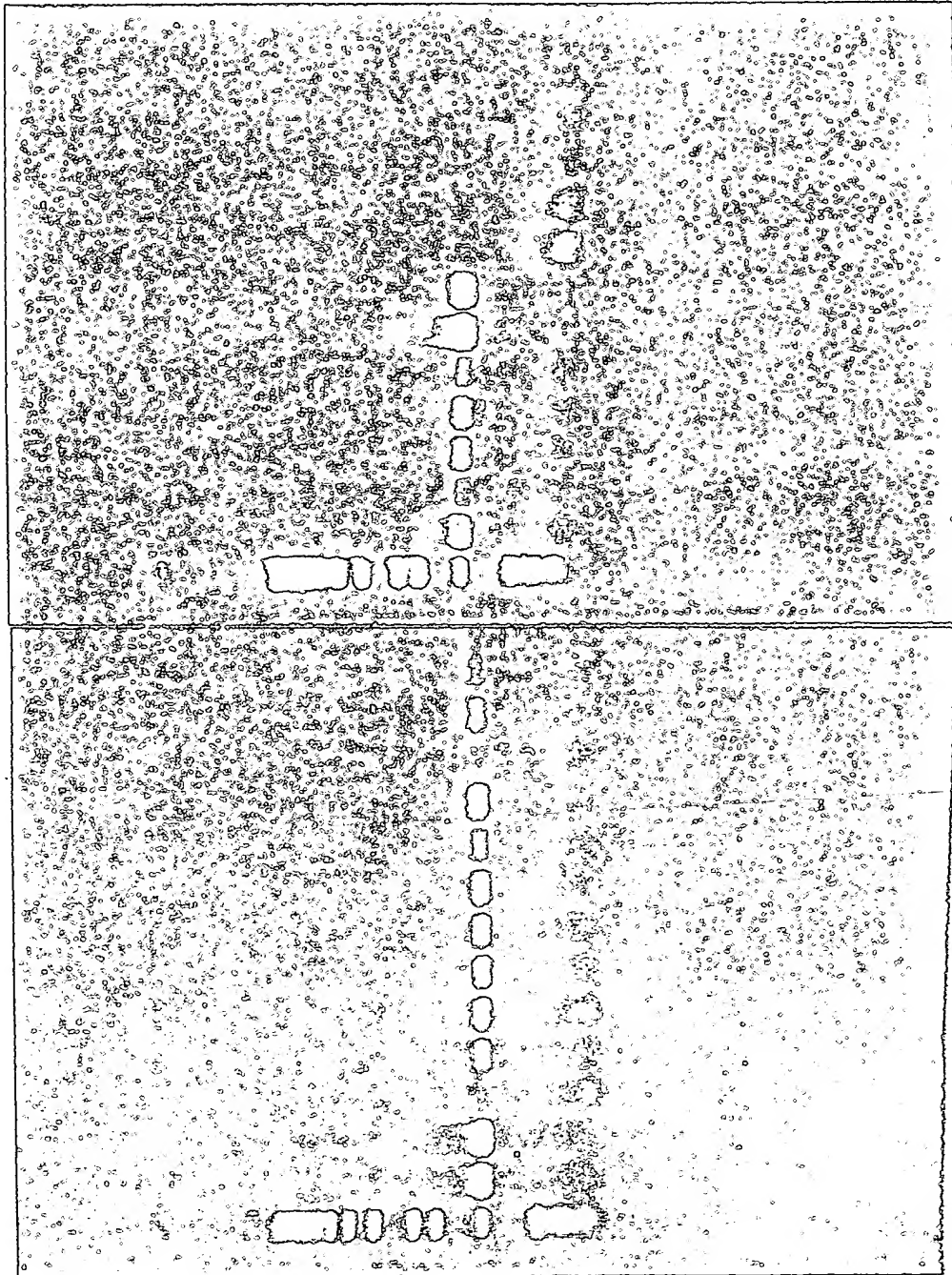
**FIGURE 11**



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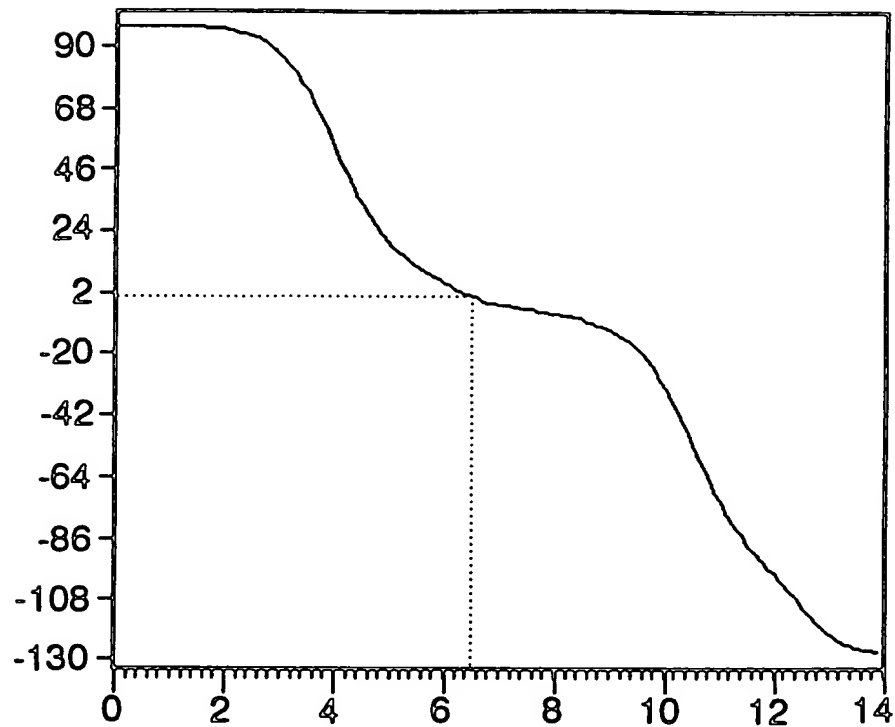
FIGURE 12B

0 1 2 3 4 5 6 7 8 9 10 11 12 13 0 14 15 16 17 18 19 20



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FIG. 13



Done on sequence PMSANTIGEN.  
Total number of residues is: 750.  
Analysis done on the complete sequence.

In Helical	(H)	conformation	[DC =	-75	CNAT ]	:	264	AA =>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT ]	:	309	AA =>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT ]	:	76	AA =>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT ]	:	101	AA =>	13.4%

Sequence shown with conformation codes.

Consecutive stretch of 5 or more residues in a given conformation are overlined.

[illegible]



**FIG. 14-3**

[illegible]

00000000000000000000000000000000



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FIG. 14-4

Semi-graphical output.  
=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNLLETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEAT				
XXXXXXXXXXXXXXXX>>>-----XXXXXXXXXXXXXXXX>X				
XXXXXXXXXXXXXXXX>>>-----XXXXXXXXXXXXXXXX>X				
60	70	80	90	100
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW				

**FIG. 14-5**

[illegible]

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FIG. 14-6

```
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--

210      220      230      240      250
|         |         |         |
VIARYGVFRGNKVNQAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG

----->>*>*>*>----->>----->>*>
----->>*>*>*>----->>----->>*>

260      270      280      290      300
|         |         |         |
GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY

>*>----->>*>*>*>-----XX-----
>*>----->>*>*>*>-----XX-----

310      320      330      340      350
|         |         |         |
DAQKLEKMGGSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKWHISTN

XXXXXXXXXX->>*>*>*>----->>----->>*>
XXXXXXXXXX->>*>*>*>----->>----->>*>

360      370      380      390      400
|         |         |         |
EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGIDPQSGAAVVHEIVR
```

[illegible]

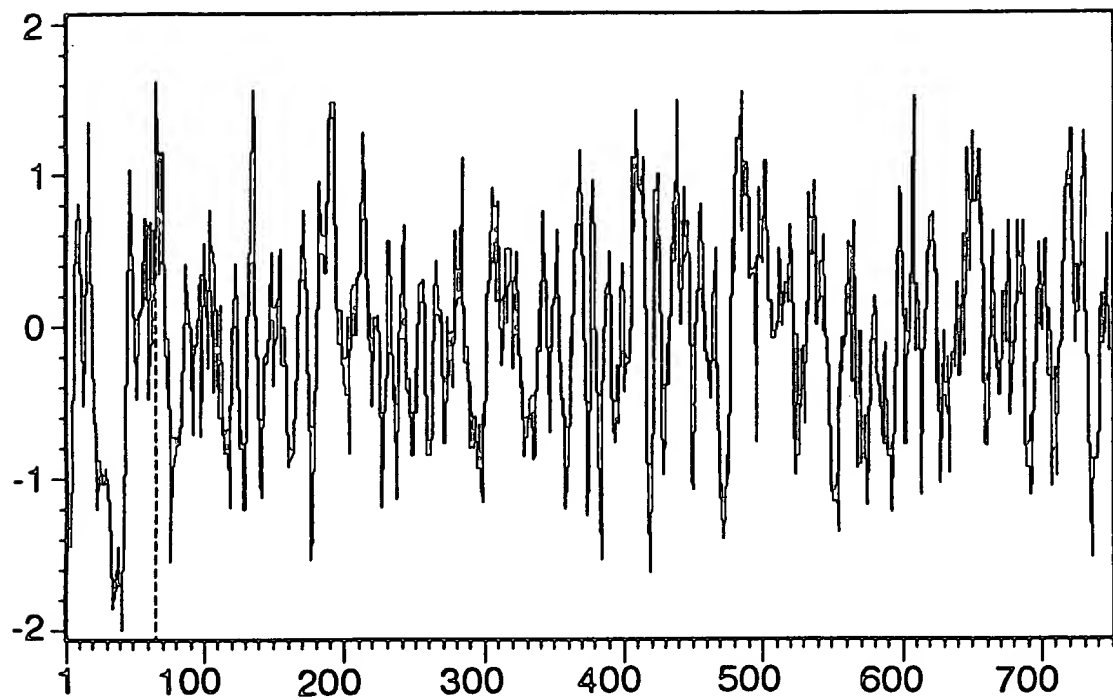
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FIG. 14-8

LYHSVETVELVEKFDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY  
-----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX  
-----XXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX  
610 620 630 640 650  
| | | | |  
AVLRYADKIYISIMKHPQEMKTYSVSFDLSFSAVKNFTETIASKFSERL  
XXXXXXXXXX-----X\*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXX-----X\*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX  
660 670 680 690 700  
| | | | |  
QDFDKSNPIVLRMTNDQIMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY  
XX>>>\*>-----XXXXXXXXXX->>>\*>----->\*\*\*>  
XX>>>\*>-----XXXXXXXXXX->>>\*>----->\*\*\*>  
710 720 730 740 750  
| | | | |  
AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAETLSEVA  
----->--XXXXXXXXXX\*\*XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX  
----->--XXXXXXXXXX\*\*XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX

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FIG. 15A



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FIG. 15B

\*\*\*\*\*  
\* PREDICTION OF ANTIGENIC DETERMINANTS \*  
\*\*\*\*\*

Done on sequence PMSANTIGEN.  
Total number of residues is: 750.  
Analysis done on the complete sequence.

The method used is that of Hopp and Woods.  
The averaging group length is: 6 amino acids.  
-> This is the value recommended by the authors <-

-----

The three highest points of hydrophilicity are:

( 1)	Ah=	1.62	:	From	63	to	68	:	Asp-Glu-Leu-Lys-Ala-Glu
( 2)	Ah=	1.57	:	From	132	to	137	:	Asn-Glu-Asp-Gly-Asn-Glu
( 3)	Ah=	1.55	:	From	482	to	487	:	Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

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FIG. 16-1

The best scores are:

CHKTFER	G.gallus mRNA for transferrin receptor	initn	initl	opt
RATTRFR	Rat transferrin receptor mRNA, 3' end.	203	120	321
HUMTFRR	Human transferrin receptor mRNA, complete cd	164	164	311
		145	145	266

CHKTFER G.gallus mRNA for transferrin receptor 203 120 321  
51.9% identity in 717 nt overlap

1020	1030	1040	1050	1060	1070
pmsgen	TGTCAGCGTGGAATAATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA				
CHKTFE	TACACTTATCCCATTCGGACATGCCACCTTGGAACCTGGAGACCCCTTACACCCAGGCTT				
990	1000	1010	1020	1030	1040

1080	1090	1100	1110	1120	1130
pmsgen	CCCAGCAATGAATATGCTTATAGCGGTGGAATTGCAGAGGCTGTGGTCTTCCAAGTAT				
CHKTFE	CCCTTCGTTCAACCACACCCCA---GTTCCACCAGTTGAATCTTCAGGACTACCCACAT				
1050	1060	1070	1080	1090	1100

1140	1150	1160	1170	1180	1190
pmsgen	TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC				
CHKTFE	TGCTGTTCAGACCATCTCTAGCAGTGCGCAGCAGCCAGGCTGTTTCAGCAAAATGATGGAGA				
1110	1120	1130	1140	1150	1160



**FIG. 16-2**

[illegible]

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FIG. 16-3

```
1440      1450      1460      1470      1480      1490
pmsgen AGCTGTTGTTCAATGAAATTGTGAG--GAGCTTTGGAACACTGAAAGGAGGAGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TGCTATATTGTTGGAACCTTGCCCGTGTGATCTCAGACATAGTGAAAAACGAGGCTACAA
1390      1400      1410      1420      1430      1440

      1500      1510      1520      1530      1540      1550
pmsgen ACCTAGAAACAATTGTTTGCAGCTGGGATGCAGAAAGAAATTGGTCTTCTTGGTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE ACCGAGCGAAGCATCATCTTTGCTAGCTGGAGTGCAGGAGACTACGGAGCTGTGGGTGC
1450      1460      1470      1480      1490      1500

      1560      1570      1580      1590      1600      1610
pmsgen TACTGAGTGGGCAGAGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTTATATAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TACTGAATGGCTGGAGGGTACTCTGCCATGCTGCATGCCAAAGCTTTCACATTACATCA-
1510      1520      1530      1540      1550      1560

      1620      1630      1640      1650      1660      1670
pmsgen TGC-TGACTCATCTATAGAAGGAACTA-CACTCTGAGAGTTGATGTACACCGCTGATG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE -GCTTGGATGCTCCAGTCCCTGGGAGCAAGCCCATGTCAAGATTTCTGCCAGCCCCCTTGCTG
1570      1580      1590      1600      1610      1620
```

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FIG. 16-4

```
1680      1690      1700      1710      1720      1730
pmsgen  TACAGCTTGGTACACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE  TATATGCTGCTGGGAGTATTATGAAGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC
1630      1640      1650      1660      1670      1680

1740      1750      1760      1770      1780      1790
pmsgen  AAATCTCTTTATGAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGCCATGCCCC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE  -----CTCTATAACAGACTTGGCCCAGACTGGGTAAAGCAGTTGTTCCCTCTTGGCCCTGGA
1690      1700      1710      1720      1730
```

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FIG. 16-5

```

RATRRF  Rat transferrin receptor mRNA, 3' end.      164  164  311
55.5% identity in 560 nt overlap

      1210      1220      1230      1240      1250
pmsgen CCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGGCTT-
      :::: :::: :::: :::: :::: :::: :::: :::: ::::
RATRRF TGCAGAAAAGCTATTCAAAAACATGGGAAGGAACTGTCTCCTAGTTGGAATATAGATTC
      610      620      630      640      650      660

      1260      1270      1280      1290      1300      1310
pmsgen -TACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG----
      :::: :::: :::: :::: :::: :::: :::: :::: ::::
RATRRF CTCATGTAAAGCTGGAACTTTTCACAGAAATCAAAATGTGAAGCTCACTGTGAACAATGTACT
      670      680      690      700      710      720

```

pmsgen --AAGTGACAAAGAATTACAAATGTGATAGGTACTCTCAGAGGAGCAGTGGAAACCAGACAG  
RATTRF GAAAGAAAACAAGAAATACTTAACATCTTTGGCGTTATTAAAGGCTATGAGGAACCAGACCG  
730 740 750 760 770 780

pmsgen ATATGTCATTCTGGGAGGTCACCCGGCACTCATGGTGTTGGTGGTATTGACCCCTCAGAG  
RATTRF CTACATTGTAGTAGGAGGCCAGAGACGCTTGGGGCCCTGGT-GTTGCCGAAGTCCAGTG  
790 800 810 820 830 840

pmsgen T-GGAGCAGCTGTTGTTTCATGAATGTGAGGAGCTTTGGAACA-CTGA--AAAAGGAA  
RATTRF TGGGAACAGGTCTT-CTGTTGAAACTTGCCCCAAGTATTTCTCAGATATGATTTCAAAGAT  
850 860 870 880 890 900

pmsgen GGTGGAGACCTAGAAGAACAAATTTGTTTGCAAGCTGGGATGCAGAACAATTGGTCTT  
RATTRF GGATTAGACCCAGCAGGAGTATTATCTTTGCCAGCTGGACTGCAGGAGACTATGGAGCT  
910 920 930 940 950 960

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FIG. 16-7

```

1550      1560      1570      1580      1590      1600
pmsgen  CTGGTCTACTAGTGGGCACAGGAGAA---TTCAAGACTCCTTCAAGAGCGTGGCGTG
      : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : :
RATRF   GTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTCATCTTTGCATCTAAAG---GCTTTC
970      980      990      1000      1010      1020

1610      1620      1630      1640      1650      1660
pmsgen  GCTTATATTAATGCTGACTCATCTATAGAAGGAACTA-CACTCTGAGAGTTGATTGTAC
      : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : :
RATRF   ACTTACATTAAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG
1030      1040      1050      1060      1070      1080

1670      1680      1690      1700      1710      1720
pmsgen  ACCGCTGATGTACAGCTTGGTACACAACCTAACAAAGAGCTGAAAGC-CCTGATGAAG
      : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : :
RATRF   CCCCCATTATATACACTTATGGGGAAGATAATGCAGGA--CGTAAAGCATCCGA-----
1090      1100      1110      1120      1130
```

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FIG. 16-8

```

1730      1740      1750      1760      1770
pmsgen GCTTTGAAGGCAAAATCTCTTTAT-GAA-----AGTTGGACTAAATAAGTCCCTTCCCCCAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
RATTRF ---TTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
1140      1150      1160      1170      1180      1190

1780      1790      1800      1810      1820      1830
pmsgen AGTCAGTGGCATGCCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTGAGGTGTTCT

RATTRF CCTTGACAATGCTGCATTCCCTTTTCTTGCAATATTCAGGAATCCCAGCAGTTTCTTTCT
1200      1210      1220      1230      1240      1250
```

HUMTFR	Human transferrin receptor mRNA, complete cd	145	145	266
54.3%	identity in 464 nt overlap			

	1400	1410	1420	1430	1440	1450
pmsgen	CCGGACTCATGGGTGTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTGTTTCATG					
	: : :	: : : : :	: : : :	: : : :	: : : : :	: : :
HUMTFR	GAGAGATGCATGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA					
1320	1330	1340	1350	1360	1370	



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FIG. 16-10

1460	1470	1480	1490	1500
pmsgen AAATTG---	TCAGGAGCTTTGGAACACTGAA	AAAGGAGGTGGAGACCTAGAA	GAAACAA	
:: :: ::	:: :: ::	:: :: ::	X :: ::	:: :: ::
HUMTFR AACTTGCCAGATGTTCTCAGATATGGTCTTAAAGATGGGTTTCAGCCAGCAGAAAGCA				
1380	1390	1400	1410	1420
1510	1520	1530	1540	1550
pmsgen TTTTGTTCGAAGCTGGGATGCAGAGAAATTGGTCTTCTTGGTCTACTGAGTGGCAG				
:: :: :: ::	:: :: ::	:: :: ::	:: :: ::	:: :: ::
HUMTFR TTATCTTTGCCAGTTGGAGTGCTGGAGACTTTGGATCGGTTGGTGCCACTGAATGGCTAG				
1440	1450	1460	1470	1480
1570	1580	1590	1600	1610
pmsgen A-GGAGAAATTCAGACTCCTTCAAGAGCGGTGGCTTATATTAATGCTGACTCATCT				
:: :: ::	:: :: ::	:: :: ::	:: :: ::	X :: ::
HUMTFR AGGATACCTTTCGTC-CCTGCATTAAAGGCTTTCACCTTATATTAATCTGGATAAAGCG				
1500	1510	1520	1530	1540
1630	1640	1650	1660	1670
pmsgen ATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC				
:: :: ::	:: :: ::	:: :: ::	:: :: ::	:: :: ::
HUMTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACGCTTATTGAG				
1560	1570	1580	1590	1600
				1610

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FIG. 16-11

1690	1700	1710	1720	1730	1740
pmshen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTTATG				
	: : : :	: : : :			
HUMTFR	AAAACAATGCACAAATGTGAAGCATCCGGTACTGGGCAATTTCATATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

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FIGURE 17A

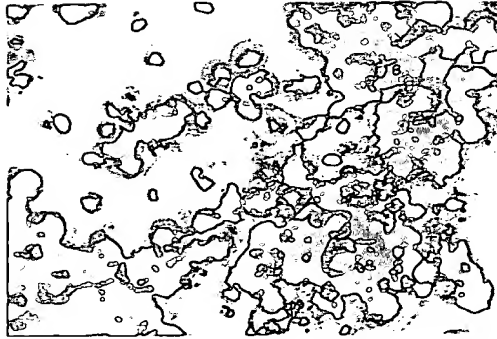


FIGURE 17B

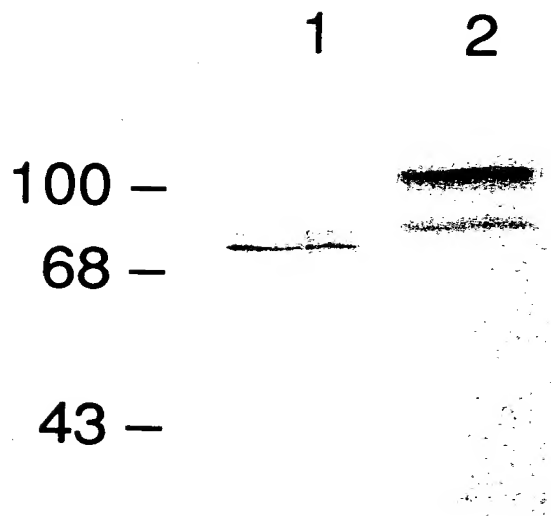


FIGURE 17C



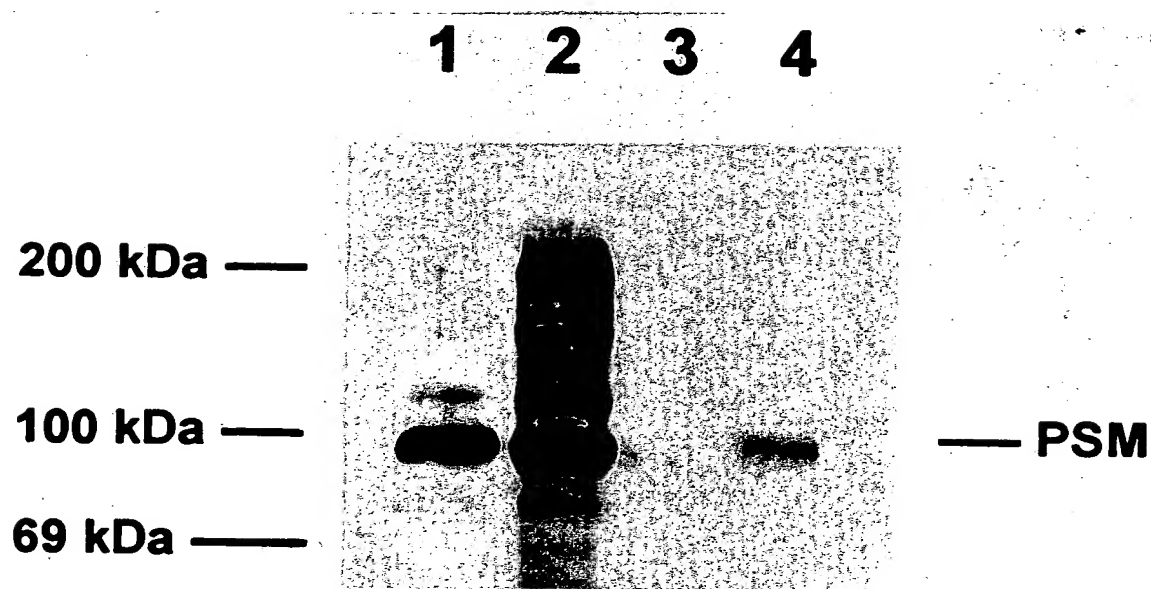
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*FIGURE 18*



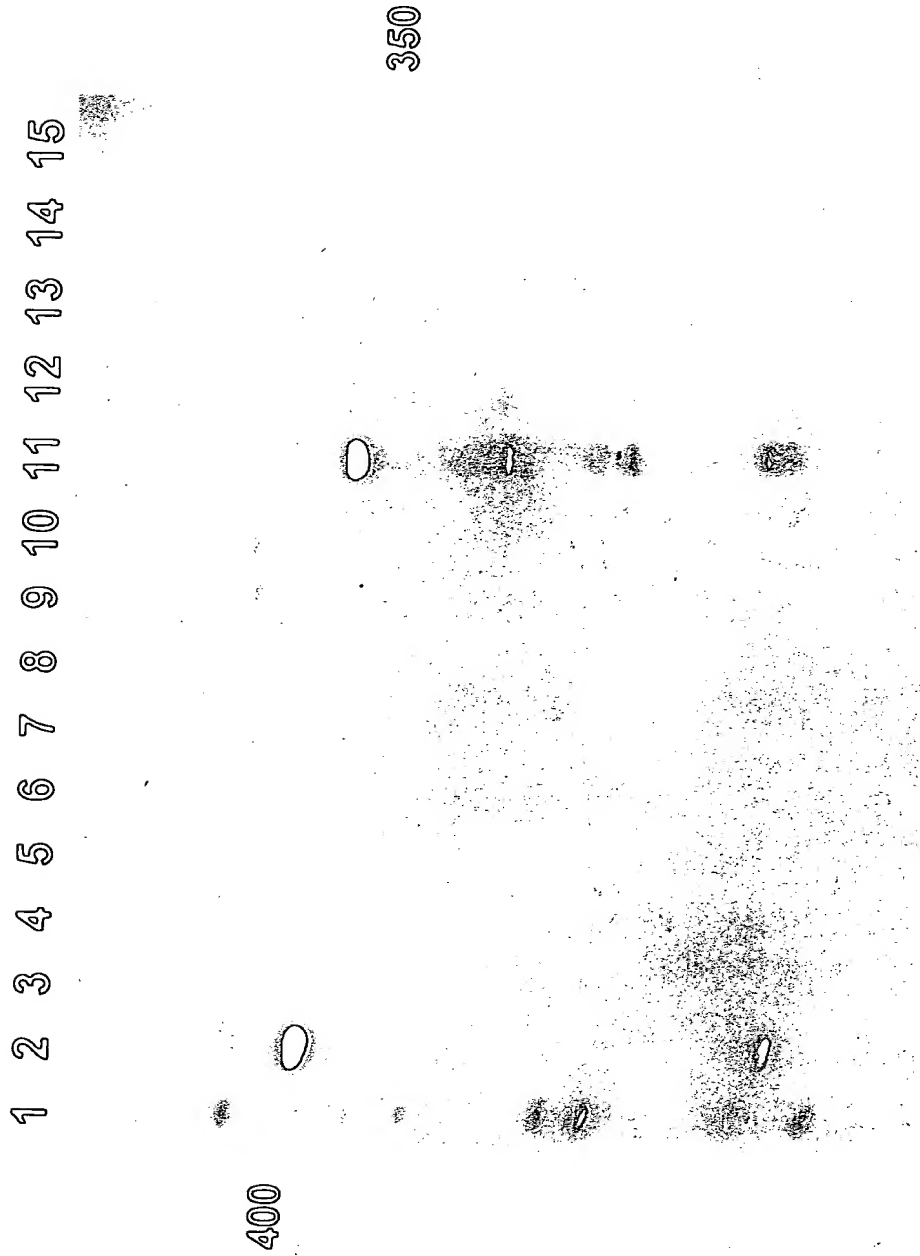
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**FIGURE 19**



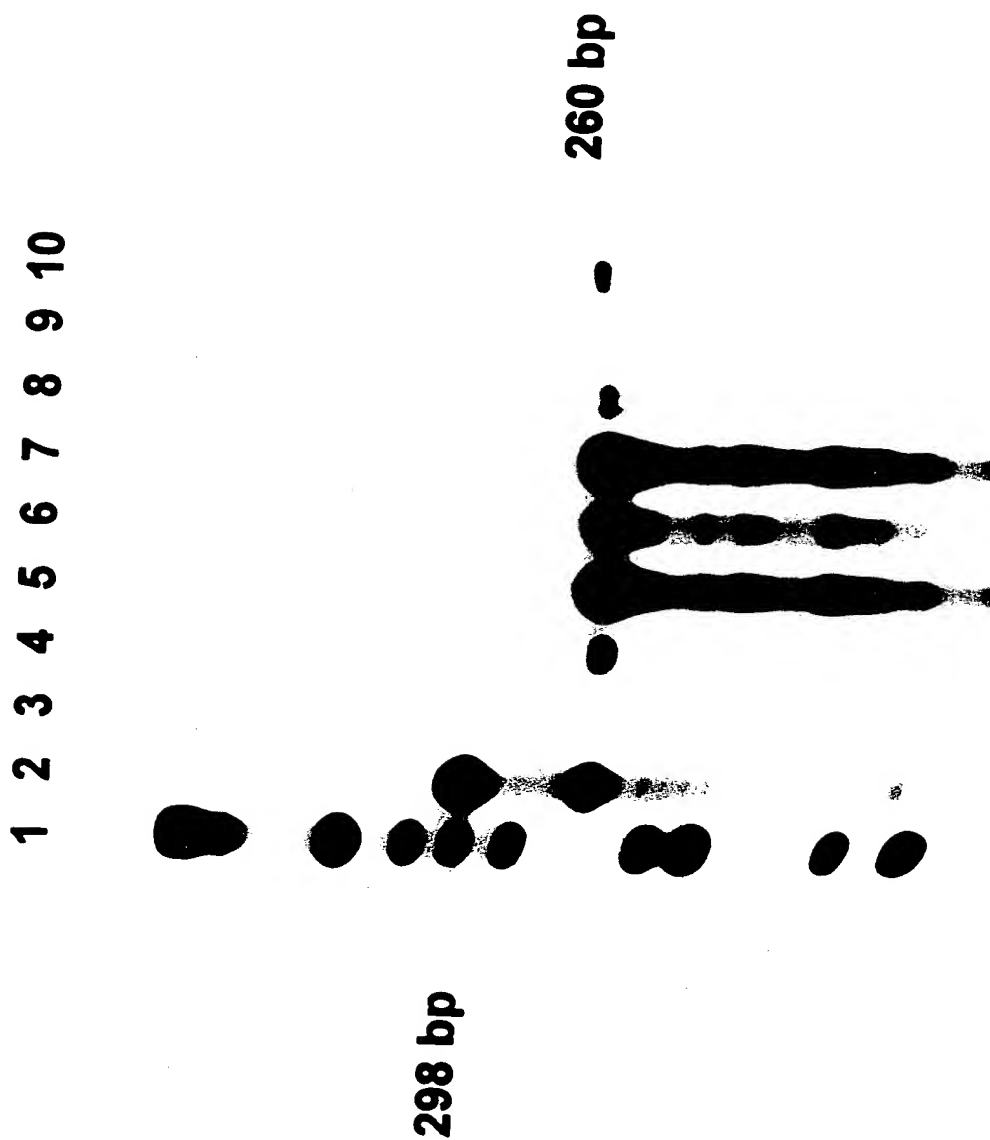
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FIGURE 20



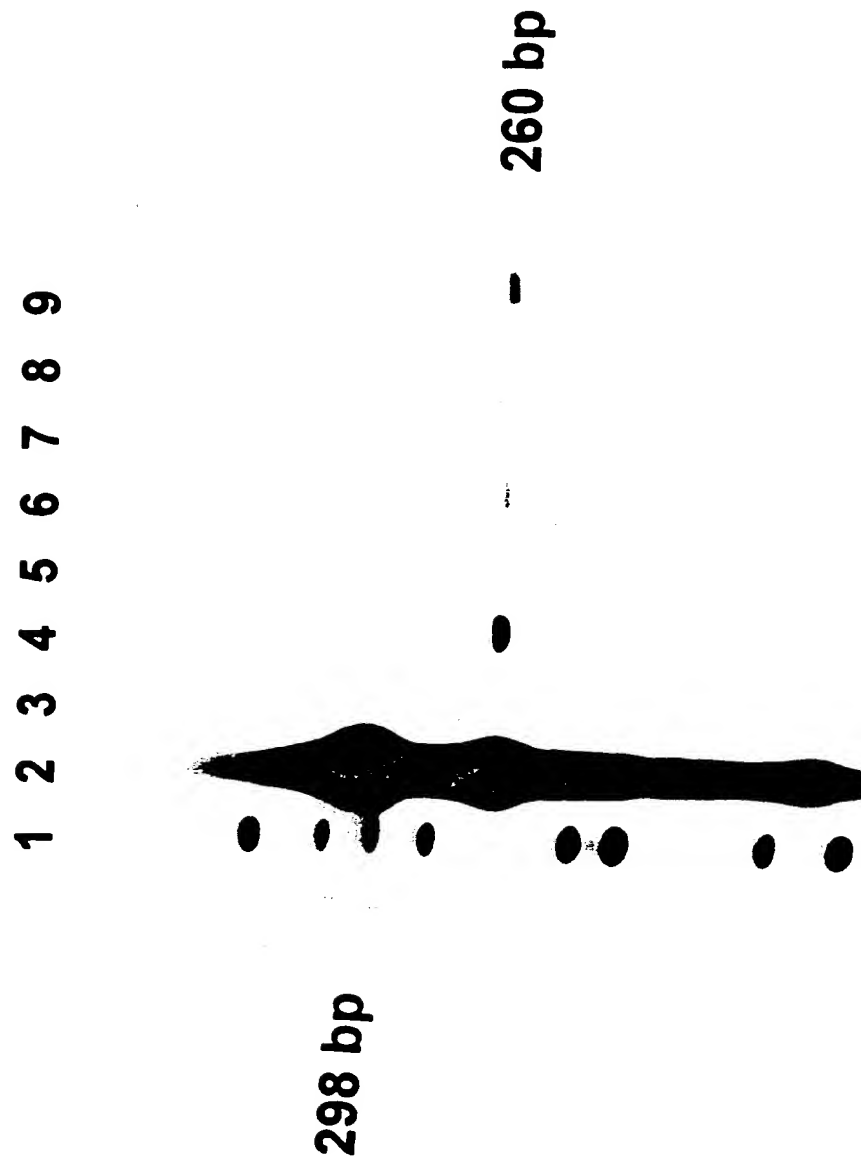
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FIGURE 21



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FIGURE 22





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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

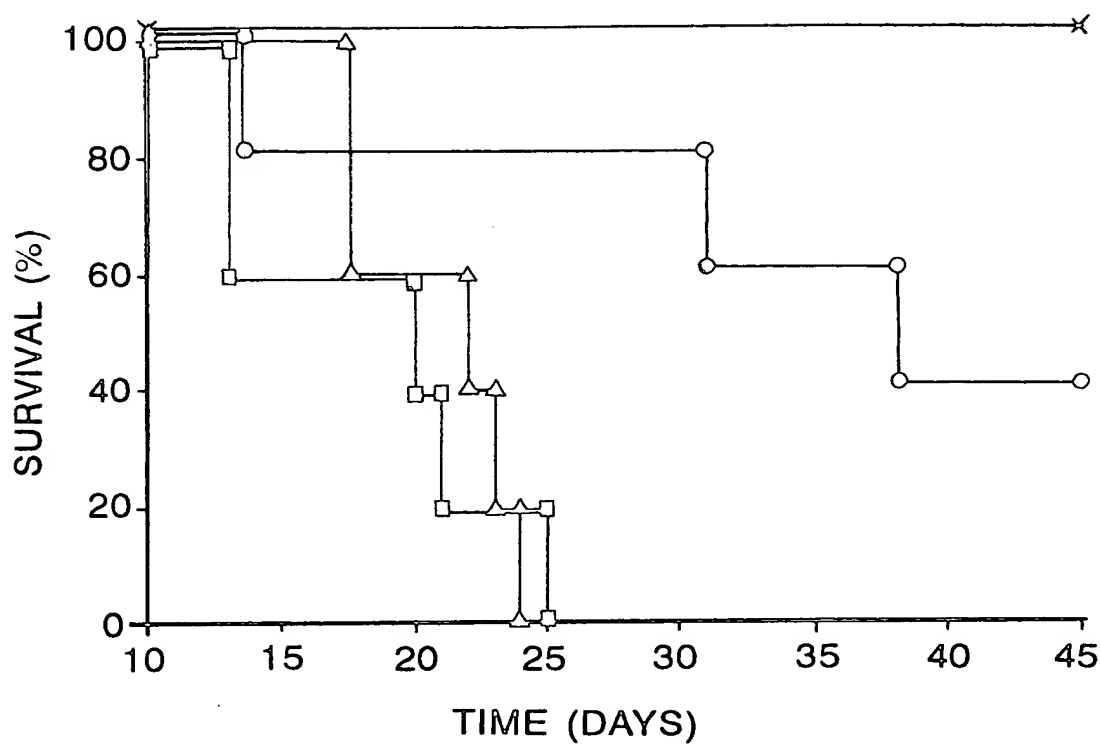
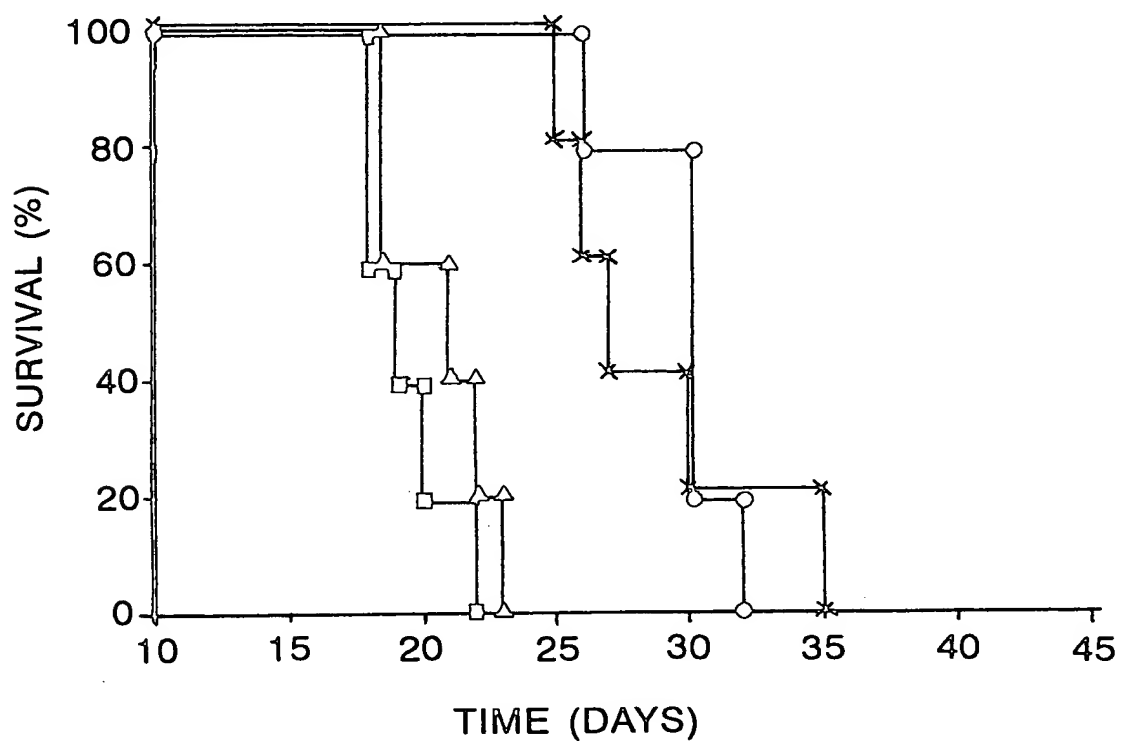


FIGURE 24B



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FIGURE 25A

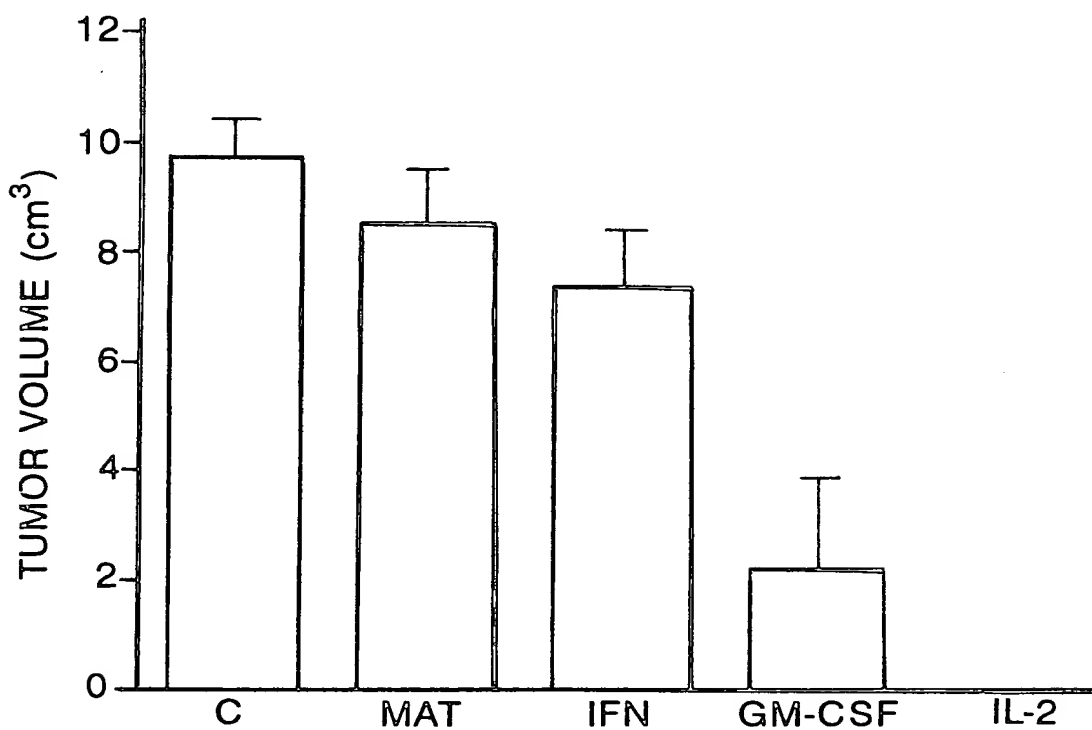
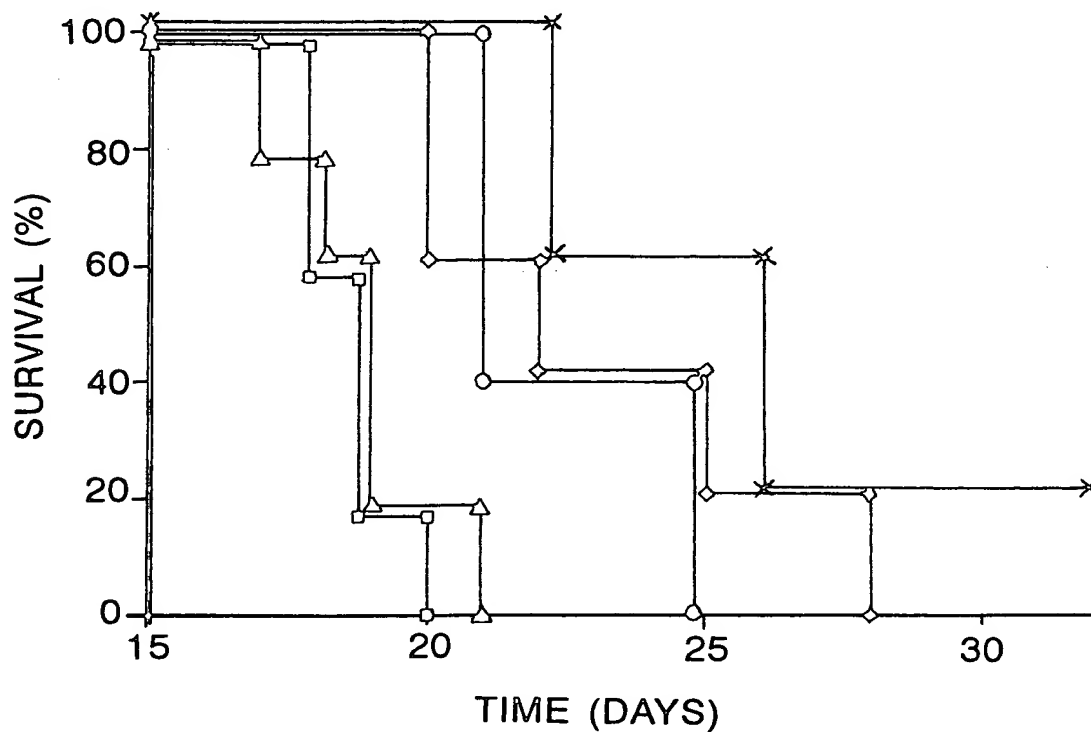
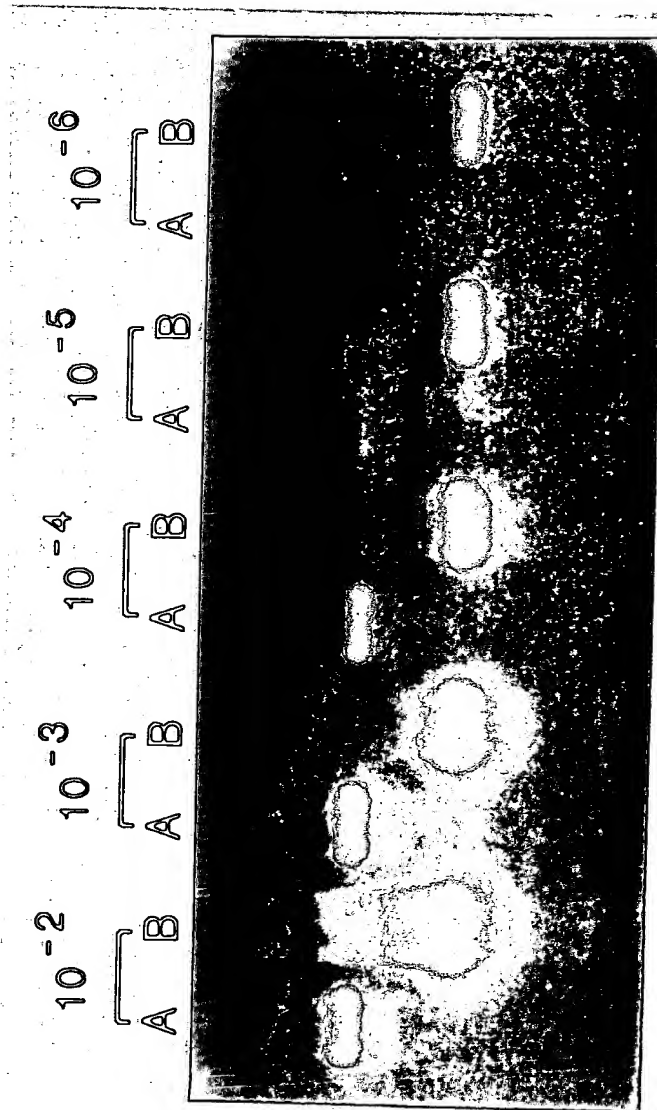


FIGURE 25B



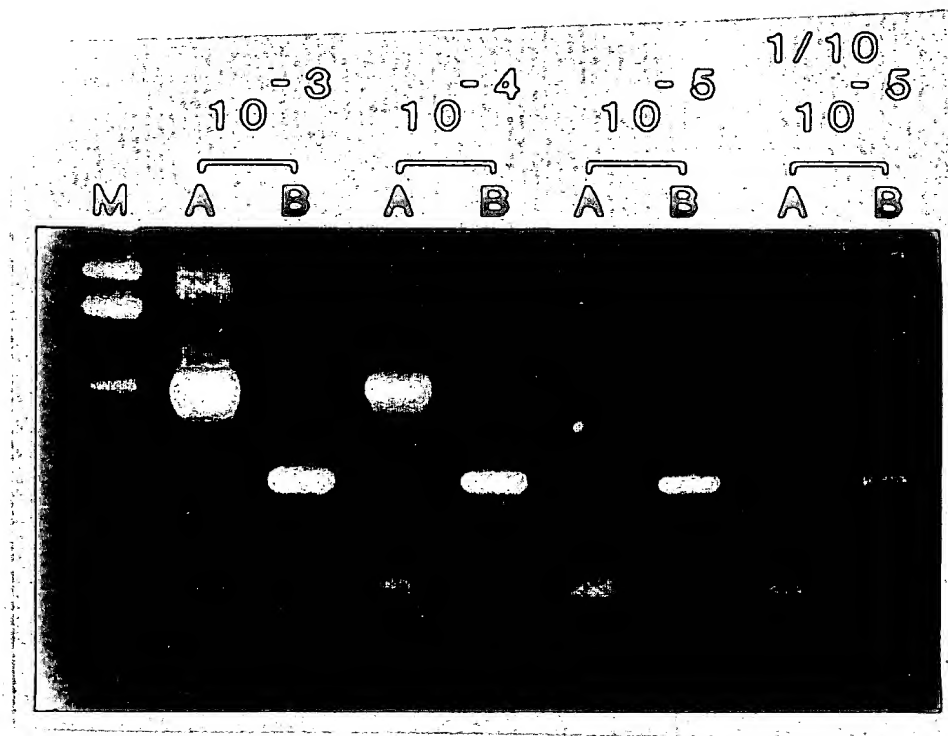
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FIGURE 26



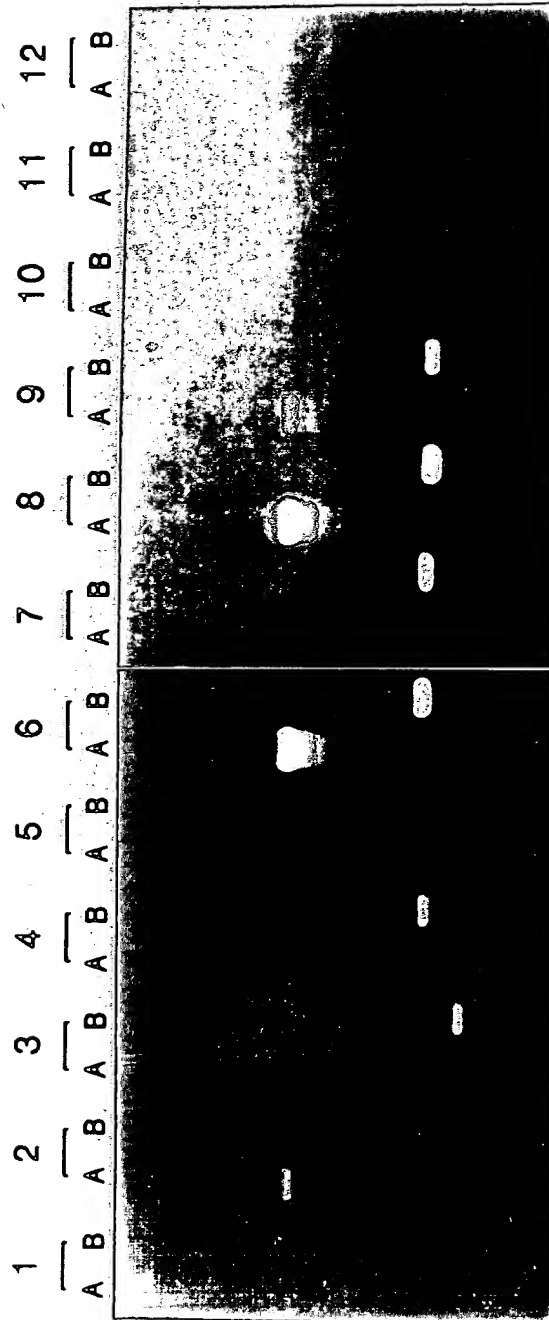
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FIGURE 27



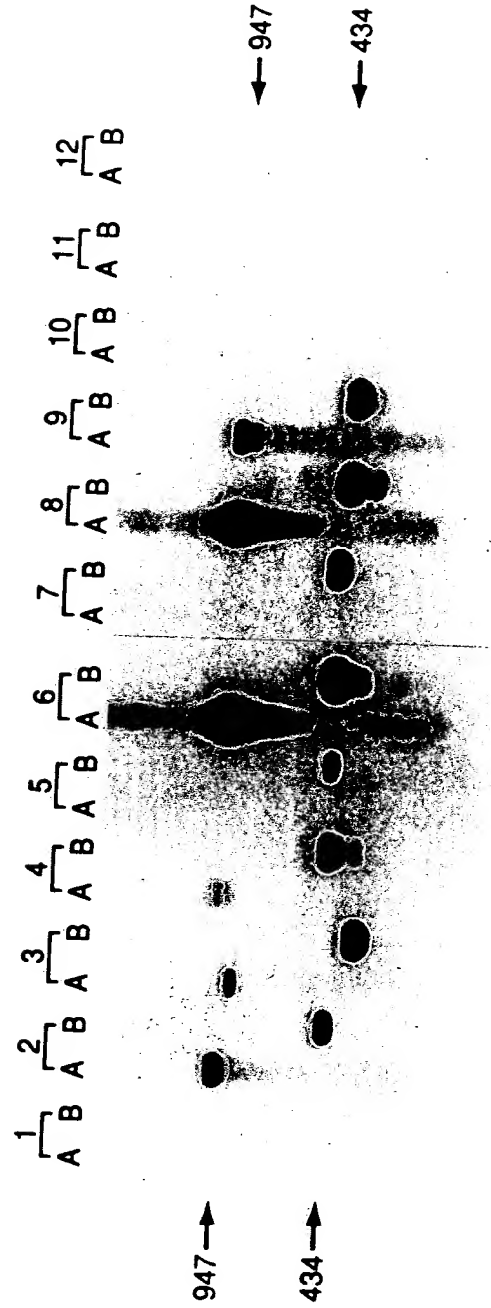
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FIGURE 28



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FIGURE 29



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*FIGURE 30*

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	—	+
2	T2NoMo	RRP 7/93	6.1	—	—	+
3	T2CNoMo	PLND 5/93	4.5	0.1	—	+
4	T2BNoMo	RRP 3/92	NMA	0.4	—	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	—	+
6	Recur T3	I-125 1986	54.7	1.4	—	+
7	T3ANoMo	RRP 10/92	NMA	0.3	—	+
8	T3NxMo	XRT 1987	7.5	0.1	—	—
9	T3NxMo	Proscar + Flutamide	35.4	0.7	—	—
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	—	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	—	—
14	D1	PLND 1989 XRT 1989	1.6	0.4	—	—
15	D1	Proscar + Flutamide	20.8	0.5	—	—
16	T2CNoMo	RRP 4/92	0.1	0.3	—	—



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